29 Sept 2021, Wednesday @ 9:00 AM

JOINT HEARING

Texas House Committee on Culture, Recreation and Tourism
Texas House Committee on Agriculture and Livestock

**** TALKING POINTS****

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- **Chairman King, Chairman Burns and committee members, good morning and thank you for the invitation. For the record, my name is Dr. Christopher M. Seabury, and I am a tenured Professor of Animal Genomics at the College of Veterinary Medicine at Texas A&M University, where I also served as the founding track leader for the graduate training program in Genomics. I have two degrees in wildlife biology and a PhD in Population Genetics; with my PhD focusing on the genetics of prion diseases and statistical genetics. I specialize in genetic improvement of livestock, for both production and disease traits. To date, this work has resulted in competitive funding exceeding $26 Million Dollars as Project Director and/or Co-Project Director; mostly from USDA. Relevant to this hearing, I invented genome-wide technologies for genetic testing in white-tailed deer, then discovered the high heritability of differences in CWD susceptibility among farmed white-tailed deer, and finally, demonstrated the high accuracy of predictions using genome-wide data for selective breeding of white-tailed deer to reduce the prevalence of CWD; where accuracy was equivalent to or better than the national scrapie eradication program.**
- **The demand on Texas A&M resources for conducting testing related to genomic predictions for CWD has been steady, as a function of 3 USDA grants and 1 TPWD grant historically, but not overwhelming; with new grants starting soon. For each test we predict the genetic merit of each white-tailed deer with respect to CWD, thus yielding numerical "scores" that reflect varying degrees of reduced susceptibility or enhanced susceptibility, for use in selective breeding. To date we have tested over 5,000 white-tailed deer, and generally plan to do tens of thousands more, nationwide.**

- **The process for conducting the tests includes collection of a biological specimen (hair, antler core, ear tissue punch), which is submitted to our laboratory service provider GeneSeek Neogen in Lincoln Nebraska. GeneSeek applies DNA from each sample (96 at a time) to my custom engineered technology, to produce genome-wide data in the form of a genetic profile for each white-tailed deer. This profile can be moderate-density data (i.e., 125,000 variable genetic markers per deer) or low-density (i.e., 50,000 variable genetic markers per deer). I then use those genetic profiles to predict the genetic merit of each deer in relation to CWD, based on the known effects of those variable genetic markers. This produces a numeric score known as a genomically-estimated breeding value which reflects whether the deer is enriched for protective genetic elements in relation to CWD, or to the contrary, where a deer is predicted to possess an overabundance of genetic elements which enhance susceptibility. In blind validation projects involving depopulated white-tailed deer, CWD positive samples were blindly and randomly mixed into multiple (independent) sample batches submitted for genetic profiling, and 89% of the CWD positive white-tailed deer were correctly flagged by my genomic prediction program (blindly), using only genome-wide data. Three different projects were performed in this manner; each with increasing accuracy, up to 89%.**
- **At present, we have more capacity for this genetic testing than demand. For example, with my existing computing infrastructure, I can literally produce predictions in the form of genomically estimated breeding values for thousands of white-tailed deer in about 2 hours or less. Moreover, I am confident that I could produce predictions for up to 50,000 white-tailed deer per day, if the data are properly formatted by our laboratory partners at GeneSeek Neogen. Currently, the largest bottleneck in the sample processing pipeline is generating the required genome-wide data (i.e., the genetic profiles), which takes about 2-3 weeks per batch-submission to GeneSeek Neogen. GeneSeek Neogen produces genetic profiles for over 6 million plant and animal samples per year, and is really the only provider for such services.**
- **There are two options for processing a test sample. For the moderate-density testing (125,000 variable genetic markers plus the prion gene data), the cost is $165 per sample. For the low-density testing (50,000 variable genetic markers plus the prion gene data), the cost is $75 per sample. Both tests provide accurate predictions. High volume could potentially drive prices down further in the future.**
- **Chairmen, this concludes my prepared remarks; thank you for your attention. I would be happy to answer any questions.**